FUTURISTIC BIOTECHNOLOGICAL APPROACHES FOR ROLE OF MICROBES IN SUSTAINABLE AGRICULTURE AND ENVIRONMENTAL POLLUTION

Abstract

Climate change and growing global population has needed increased demand for sustainable agricultural practices. Researchers and scientists are exploring innovative solutions to enhance agricultural productivity with minimal hazardous impact on environment. Beneficial microorganisms have emerged as promising candidates in this pursuit where potentially important microbes includes *Rhodococcus* strains that showed exceptional properties to produce biosurfactants, enabling fine-tuning for soil remediation and oil spill treatment. They contribute to the circular economy by converting waste materials into valuable extracellular glycolipids. Genetic engineering techniques further enhance biosurfactant yields, offering new drives in sustainable agriculture. *Azotobacter*, a nitrogen-fixing bacterium, efficiently converts atmospheric nitrogen into ammonia, providing an eco-friendly alternative to nitrogen-based fertilizers. It also produces plant growth-promoting substances that regulate plant development, improve nutrient uptake, and enhance resistance to environmental stresses. *Bacillus subtilis*, a biofilm-forming *Rhizobacterium*, stimulates plant growth through the production of volatile organic compounds (VOCs) and siderophores, promoting nutrient availability for plants. *Bacillus subtilis'* metabolic capabilities and stress-response genes offer potential applications in organic farming and biotechnology. To address climate change's impact on agriculture, researchers and farmers are exploring innovative solutions, including the use of beneficial

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microorganisms as biofertilizers. *Rhodopseudomonas palustris*, a phototropic purple non-sulfur bacterium, shows promise in enhancing the plant growth, nutrient uptake efficiency, and soil contamination reduction. Siderophores, iron-chelating molecules, play crucial roles in regulating iron uptake by bacteria and plants. Heterobactins produced by *Rhodococcus spp*. have potential for iron sequestration and microbial interactions. However, implementation of genetic engineering tools can increase siderophore production, improving nutrient uptake and crop yields. Beneficial strains like *Mst* 8.2 and *Alcaligenes faecalis* enhance pathogen resistance and nutrient uptake in genetically modified crops, contributing to environmental sustainability and ecosystem health. In view of such important properties of these microbes we have attempted to summarize the agriculture and industrial values of bio-economical microbes and their respective byproducts.

Keywords: Agriculture, Bioremediation, Fermentation, Genetic-Engineering, Microbes, Pollution.

I. INTRODUCTION

Researchers and scientists have been exploring a wide variety of novel solutions as the world struggles to meet the pressing need for sustainable agricultural practises in the face of climate change and an ever-increasing global population. The use of beneficial microorganisms is one solution that has shown promise for increasing agricultural output with minimal negative effects on the environment[1]. The versatile *Rhodococcus* strains are one such group of microorganisms that has garnered a lot of interest because of their remarkable potential in biosurfactant production, which has many uses in environmentally friendly farming[2].

To ensure environmental health, natural resource conservation, and long-term food supply, sustainable agriculture is more important than ever. In this respect, *Rhodococcus* strains have emerged as leaders due to their extraordinary biosurfactant production abilities[3]. Their one-of-a-kind synthesis route permits fine-tuning of biosurfactant production, leading to exceptional solubilization properties well suited for soil remediation and oil spill treatment. This eco-friendly option provides a step forward in the pursuit of sustainable agricultural practises, as it may be used to clean up polluted soils with minimal environmental impact. Because of their potential to transform inexpensive and renewable waste materials into valuable extracellular glycolipids, strains hold a lot of promise in the field of sustainable agriculture[3]. Through the manipulation of metabolic pathways and the fortification of resistance to environmental challenges, genetic engineering techniques hold the promise of increasing biosurfactant yields[4]. The potential usage of the members of genus *Rhodococcus* in agriculture and environmental remediation has accredited, as scientists refine biosurfactant production[5].

Another promising player in the world of beneficial microorganisms is *Azotobacter* that offers many contributions to ecological health and agricultural sustainability[6]. *Azotobacter*, a type of nitrogen-fixing bacterium, can convert nitrogen in the air into usable ammonia, making it a more environmentally friendly fertiliser [7]. *Azotobacter*-inoculated crops provide a more sustainable and economical alternative to conventional farming by reducing the need for synthetic fertilisers[8]. As the world's population rises, the need for the agricultural sector to make use of beneficial microorganisms has become a pressing need. Biofilm-forming Rhizobacterium *Bacillus subtilis* is well-known for its ability to promote plant growth via the release of volatile organic compounds (VOCs). These VOCs improve plant growth and health by increasing photosynthetic activity and stimulating the production of phytohormones[9]. With their arsenal of stress-regulation and plant-growth genes, *Bacillus* species offer a promising new direction for genetic engineering and stress-management techniques[10]. Root rhizosphere bacterial growth and biofilm formation enable beneficial interactions that improve plant growth and stress tolerance[11].

When considering biofertilizers, the phototropic purple non-sulfur bacterium (PNSB) *Rhodopseudomonas palustris* stands out as a strong contender due to its potential to boost plant growth, increase nutrient uptake efficiency, and reduce soil contamination[12]. Understanding and addressing potential barriers to adoption is crucial to the successful implementation of *R. palustris* as a biofertilizer[13]. We can smooth the way for the incorporation of this remarkable bacterium into sustainable farming practises by conducting thorough social and economic research. Siderophores, iron-chelating molecules, have been

shown to play a critical role in controlling iron uptake and nutrient availability in both bacteria and plants[14]. *Rhodococcus spp*. produce an interesting class of heterobactins with mixed catecholate-hydroxamate structures that contribute to the expansion of sustainable agriculture[15]. Improvements in nutrient uptake and crop yields may be achieved through genetic engineering's potential to enhance siderophore production[16]. In order to improve pathogen resistance and nutrient uptake in genetically modified crops, beneficial strains such as *Mst 8.2* and *Alcaligenes faecalis* have been shown to be effective[17]. As an added bonus, siderophores may prove to be a game-changer in the field of phytoremediation by providing a long-term solution to the problem of heavy metal pollution and the promotion of ecosystem health. Understanding the processes of action, optimising production, and studying the impact on crops are all vital to creating a more secure food supply[18].
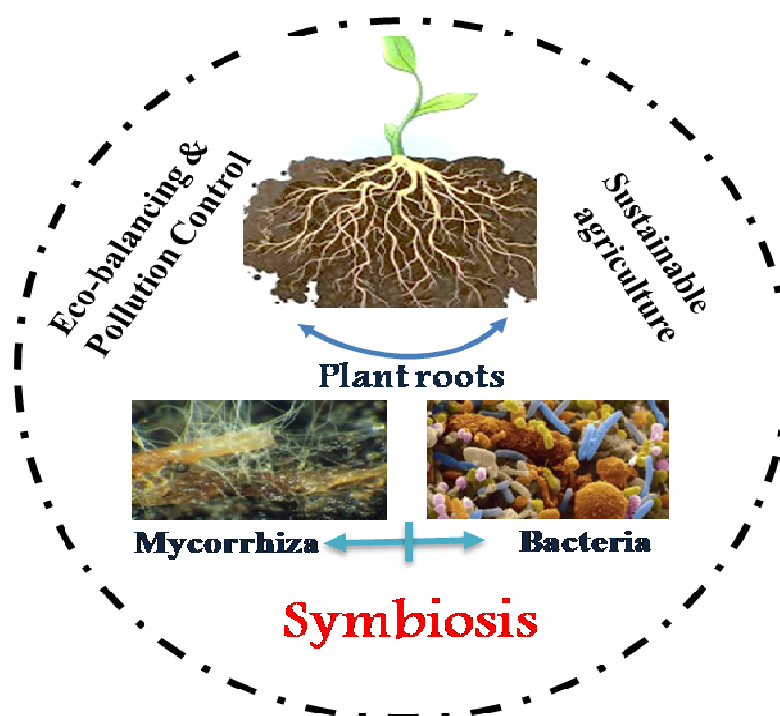

Illustration: Overview of Microbe-Plant Symbiosis for Sustainable Agriculture and Eco-Balancing/Pollution Control

II. RHODOCOCCUS AS A POTENTIAL BIOSURFACTANT MICROBE

Biosurfactants are a kind of surfactant that degrades over time and has several benefits over traditional surfactants, including a lower critical micelle concentration (CMC), less toxicity, and increased stability. They are made by many species of the genus *Rhodococcus* and may be obtained from sustainable resources. These biosurfactants work well with both hydrocarbon-based and alcohol- and sugar-based substrates, demonstrating their versatility. Trehalolipids, which are based on the sugar trehalose, are one kind of biosurfactant generated by *Rhodococcus*[19]. Uses of TP compounds in the cosmetics and food industries are only the tip of the iceberg when it comes to their environmental benefits. These molecules also have beneficial medicinal features, such as the ability to stimulate the immune system and fight cancer and viruses. Benefits of biosurfactants in agriculture include

enhanced nutrient absorption and soil remediation[20]. Microorganisms are responsible for the generation of naturally occurring surface-active chemicals[21]. Growth substrate and cell growth phase affect biosurfactant synthesis in *Rhodococcus* strains[22]. Recovering these biosurfactants for commercial usage may be tricky since they can exist in two distinct forms: extracellular and cell-bound. Biosurfactant synthesis is regulated in different *Rhodococcus* strains by a variety of factors, including the kind of growth substrate used[23]. Significantly less hazardous than synthetic commercial surfactants, *Rhodococcus* biosurfactants have shown their worth in solubilizing polyaromatic hydrocarbons[24]. Researchers have been looking for ways to lower the price of biosurfactant manufacturing by using inexpensive substrates like industrial and municipal wastes. Some *Rhodococcus* strains, for instance, have been shown to produce extracellular glycolipids from renewable resources like sunflower frying oil. *Rhodococcus* strains have been proven in interesting studies to produce biosurfactant on a wide variety of substrates, including rapeseed oil and fish waste compost[25]. More research is needed to fully understand the genetics and biochemistry of *Rhodococcus* strains, which are responsible for biosurfactant synthesis. Factors such as growth substrate and cell development phase affect *Rhodococcus* strains' ability to produce biosurfactants[26], thus it's important to take them into account. The development of anionic trehalose tetra-esters, for instance, has been linked to nitrogen restriction[27]. Different biosurfactant molecules may be synthesised if the cells are given different growth substrates. Succinoyl trehalose lipids with acyl groups of the same carbon chain length as the growth substrate may be biosynthesized when *Rhodococcus* cells are fed various n-alkanes[24]. Compared to many synthetic surfactants, biosurfactants from the *Rhodococcus* species have lower critical micelle concentrations and are more efficient in reducing surface and interfacial tensions between aqueous and oil phases (CMCs)[2]. Biosurfactant manufacturing utilising *Rhodococcus* strains may be somewhat costly, hence efforts have been made to find inexpensive substrates, such as used sunflower frying oil, rapeseed oil, and composted fish waste. *Rhodococcus* strains can grow well on these substrates, and biosurfactant synthesis is facilitated.

To improve the production of biosurfactants using *Rhodococcus* bacterial strains, several strategies can be employed. These strategies aim to enhance productivity, optimize resources, and promote environmental sustainability[28]. Genetic engineering techniques can be applied to modify the metabolic pathways of *Rhodococcus* strains. By introducing genetic modifications, it is possible to optimize the biosurfactant production pathways, leading to increased yields. This approach allows for tailored enhancements in the strain's biosurfactant production capabilities[29]. The choice of cost-effective substrates becomes crucial. Therefore, identifying and utilizing substrates that are economically viable and suitable for *Rhodococcus* growth and biosurfactant production is essential. Such substrates should provide the necessary nutrients and support robust biosurfactant yields while minimizing production costs[30]. Optimizing the growth media formulation is another critical factor. Developing an optimized media composition that fulfils the nutritional requirements of *Rhodococcus* strains and creates a favourable growth environment can significantly improve biosurfactant production[31]. Innovative statistical approaches, like surface methodology, can be employed to optimize the media composition and relevant parameters.Furthermore, improvements in the fermentation process can be achieved by controlling and optimizing parameters such as temperature, pH, oxygen levels, and agitation. Creating an ideal fermentation environment promotes the growth of *Rhodococcus* strains and enhances biosurfactant production. Monitoring and adjusting these parameters based on well-developed

statistical models can optimize the fermentation process[32]. Efficient downstream processing and purification methods should be developed to extract and purify biosurfactants from the *Rhodococcus* fermentation broth. Techniques such as chromatography, membrane filtration, and solvent extraction can be employed to achieve high-quality and purified biosurfactant products. The utilization of well-developed statistical models is essential. These models aid in understanding the biosurfactant production process using *Rhodococcus* strains. They help identify critical process parameters, optimize production conditions, and predict outcomes, leading to improved process efficiency and cost-effectiveness[33].

However, utilizing waste products as carbon sources for biosurfactant production can be advantageous. *Rhodococcus* strains can be cultivated using carbon-rich waste materials such as vegetable oils, oil residues, dairy products, and distillery residues. This approach not only reduces production costs but also contributes to a circular economy by repurposing waste materials[34]. Optimizing the combination of carbon substrates can enhance biosurfactant production in *Rhodococcus* strains. Studies have shown that combining hydrophobic and hydrophilic carbon sources, such as glucose and vegetable oil, at concentrations above 5%, can lead to increased biosurfactant productivity in yeast strains[35]. Similarly, exploring different combinations of carbon substrates, particularly focusing on hydrophobic sources, may improve biosurfactant production in *Rhodococcus* strains[36]. Furthermore, considering the molecular weight of carbon sources can influence biosurfactant yield. Supplementing the growth medium with glycerol (three-carbon organic compound), that can be easily metabolized by *Rhodococcus* and other bacteria, has been reported to increase biosurfactant production[31]. Thus, optimizing the concentration and availability of glycerol as a carbon source could potentially enhance biosurfactant yield in *Rhodococcus* strains.

To maximize the potential of *Rhodococcus* strains in agriculture, a crucial approach involves optimizing the availability and ratios of nutrients, specifically the carbon-to-nitrogen (C:N) ratio. Selecting an appropriate nitrogen source is vital for microbial growth and the synthesis of valuable metabolites like biosurfactants. By simultaneously introducing organic (e.g., yeast extract) and inorganic (e.g., ammonium nitrate) nitrogen sources, conditions of limited nitrogen can be simulated, resulting in the production of biosurfactants with favourable surface tension properties[37]. Moreover, the presence and proportions of other nutrients, such as phosphorus, manganese, sulphur, and iron (notably C:N, C:Fe, and C:P ratios), significantly influence the fermentative processes leading to biosurfactant production[38]. Optimizing these parameters becomes crucial for cost-effective large-scale biosurfactant production. The C:N ratio holds particular importance in the biosurfactant production process. Higher C:N ratios can hinder microbial growth and encourage the redirection of cell metabolism toward increased biosurfactant production[39]. Consequently, it becomes essential to fine-tune the C:N ratio, emphasizing lower nitrogen concentrations, to achieve optimal biosurfactant yields. Various studies have demonstrated optimized C:N ratios for different bacterial strains, such as 7:1 for *Pseudomonas aeruginosa* F23, 22:1 for *P. nitroreducens*, and 10:1 for *Virgibacillus salarius* KSA-T[40]. Additionally, researchers have explored the impact of the oil-to-glucose ratio, finding an optimal ratio of 40:1 for biosurfactant production by *P. aeruginosa* SP4 in a mineral medium containing palm oil and glucose[41]. Furthermore, factors such as incubation time and inoculum size influence biosurfactant production. The optimal incubation time varies between bacterial strains, ranging from 18 to 48 hours, although longer times have also been reported[42]. Inoculum

size, on the other hand, can affect the yield and duration of biosurfactant production. A higher cell density achieved through a larger inoculum can favour maximum metabolite productivity, but it is crucial to balance the inoculum concentration to avoid nutrient depletion and reduced microbial activity. By considering these strategies and optimizing the nutrient availability and ratios, particularly the C:N ratio, the biosurfactant production potential of *Rhodococcus* strains can be harnessed for agricultural applications[23]. Fine-tuning the nitrogen source, adjusting nutrient ratios, and optimizing incubation time and inoculum size can enhance biosurfactant production and make *Rhodococcus* strains a promising solution in the agricultural sector. Further research and experimentation are needed to validate and optimize these strategies specifically for *Rhodococcus* strains in the context of agricultural applications.

Applying recombinant DNA technology to improve the *Rhodococcus* strain can offer numerous benefits, including higher biosurfactant yields, cost-effectiveness, and enhanced chemical properties. Using recombinant technology, microbial strains can be genetically manipulated to create biomolecules with higher efficiency and resistance to demanding environmental circumstances, such as high temperatures, salinity variations, and pH swings. Due to their versatility, they are ideally suited for agricultural applications where durability is essential. Biosurfactant production was compared between a recombinant *Escherichia coli* strain harbouring the BioS gene, srfA, and biosurfactants generated from the original *Bacillus sp.* SK320 [43]. Results demonstrated a considerable increase in biosurfactant production in the recombinant strain, demonstrating the potential of recombinant technology to increase biosurfactant yields. Similar hopeful results were reported that the biosurfactant output of a recombinant strain was double that of its parent strain. These studies demonstrate the importance of recombinant technology in increasing biosurfactant production and its application in agricultural contexts[43]. *Rhodococcus* strains can be engineered using recombinant DNA technology to optimize biosurfactant production.

By introducing specific genes or modifying metabolic pathways, the biosurfactant production capabilities of *Rhodococcus* can be enhanced. This genetic modification can lead to increased biosurfactant yields and improved performance under challenging environmental conditions[24, 33]. Furthermore, the modularization of metabolic pathways has been successfully implemented in biotechnological production to improve biosurfactant titre and yield. Wu et al. have demonstrated the effectiveness of this approach,by breaking down the biosynthetic pathways into modules, optimization and fine-tuning of specific steps become more feasible and resulted in improved biosurfactant production[44]. Employing leveraging recombinant DNA technology and applying these concepts to *Rhodococcus* strains, it is possible to enhance biosurfactant production, improve yields, and tailor their properties to meet the specific requirements of the agricultural sector[20, 28]. This can make *Rhodococcus* strains a potential candidate for sustainable agricultural practices, where the application of biosurfactants can contribute to improved soil health, enhanced nutrient availability, and other beneficial effects on crop growth and sustainability. However, further research and experimentation are needed to validate and optimize these strategies specifically for *Rhodococcus* strains in the context of agricultural applications. Leveraging the knowledge about the different routes of surfactant synthesis and their dependence on carbon sources, we can explore the potential of the *Rhodococcus* genus for agricultural applications. In the case of *Rhodococcus*, the utilization of specific carbon sources can direct biosurfactant production through different routes. For instance, by providing carbon substrates that promote both

carbohydrate and lipid synthesis simultaneously (Route A), we can enhance the production of biosurfactants. Alternatively, adjusting the carbon substrate chain length in the medium can induce lipid synthesis while the carbohydrate part is synthesized independently (Route B)[38]. Furthermore, we can employ specific carbon sources that encourage lipid synthesis while the carbohydrate part depends on the substrate used (Route C). Alternatively, by employing carbon sources that stimulate both carbohydrate and lipid synthesis (Route D), we can achieve a balanced production of biosurfactants[35]. Optimizing the culture medium and selecting appropriate carbon sources for *Rhodococcus* strains can significantly impact biosurfactant synthesis[45]. By understanding the diverse metabolic pathways involved and their dependence on the nature of the carbon sources, we can tailor biosurfactant production in *Rhodococcus* for agricultural applications. Biosurfactants produced by *Rhodococcus* can contribute to soil health, improve nutrient availability, enhance plant-microbe interactions, and potentially mitigate the use of chemical fertilizers and pesticides. Further research and experimentation are required to precisely determine the optimal carbon sources, culture conditions, and biosurfactant production routes in *Rhodococcus* strains for agricultural applications[28].

III. APPLICATIONS OF AZOTOBACTER IN SUSTAINABLE AGRICULTURE AND ECOSPHERE BALANCING

Brakel and Hilger (1965) revealed through in-vitro research that *Azotobacteria* produce indol-3-acetic acid (IAA) when tryptophan is added to the medium[46]. Hennequin and Blachère (1966) detected negligible levels of IAA in old cultures devoid of tryptophan[47]. *A. chroococcum* cultures were discovered to possess both auxin and gibberellin-like chemicals[48]. In a single *A. chroococcum* strain, Brown et al. (1968) discovered three gibberellin-like compounds, whereas Nieto and Frankenberger (1989) recognised five cytokinins[46]. It was also found that auxins, cytokinins, and GA-like compounds were produced by *Azotobacter* bacteria to promote plant development [49]. To further comprehend the IAA-producing metabolic pathways of *Azotobacterial*, additional genetic study is required, especially the identification of the genes involved in tryptophan use and IAA production in this strain. By manipulating the strain genetically, we can increase IAA production without the use of exogenous tryptophan by increasing the expression of these genes. Tryptophan and its precursors are needed, so it's important to look into the possibility of co-culturing *Azotobacteria* with other microorganisms. Synergistic interactions between members of microbial consortiums allow for more stable and long-term IAA production.

1. **Nitrogen Fixation:** Due to their quick development and capacity to fix nitrogen, azotobacteria are extremely useful as bioinoculants and are of significant interest to nitrogen fixation researchers[6]. *Azotobacter* performs a key function in supplying plants with important nutrients by turning air nitrogen into ammonia[50]. As Soleimanzadeh and Gooshchi (2013) showed, the presence of nitrogen can have a deleterious effect on the activity of *Azotobacter*[51]. *Azotobacter* has the capacity to fix up to 20 kg of nitrogen per hectare per year, making it an attractive alternative to inorganic nitrogen fertilisers for crop development [52]. As a result of using *Azotobacter* as an inoculant in crops, nitrogen fertiliser requirements can be lowered. Romero-Perdomo et al. (2017) found that a mixed culture of *Azotobacter* strains resulted in a 50 percent reduction of N-fertilizer use, highlighting its practical importance in sustainable agriculture[53]. *Azotobacter's*

inhibition by nitrogen reduces its ability to fix nitrogen for plants, leading to nitrogen deficiency in the soil. This deficiency negatively affects plant growth, chlorophyll synthesis, protein production, and enzyme activity, resulting in stunted growth, yellowing leaves, and poor crop yields. Additionally, *Azotobacter's* suppressed activity affects overall nutrient cycling, impacting the availability of essential nutrients for plant uptake. Excess nitrogen may promote the dominance of less beneficial microorganisms, disrupting the soil's microbial community balance. So, it is important to avoid over-application of nitrogen fertilizers to prevent nitrogen saturation and minimize the inhibition of nitrogen-fixing bacteria like *Azotobacter*.

2. **Siderophore Production:** Despite the availability of over 500 siderophores, only a handful are used by *Azotobacteria* to sequester iron[54]. The development of Fe-siderophore complexes may render iron less accessible to other microbes, indicating the possibility of anti-phytopathogenic qualities that protect plants against diseases and boost overall plant growth[55]. In addition to their iron-binding properties, the siderophores of *A. vinelandii* may also bind to metals other than iron. This property enables nitrogenases to absorb molybdenum (Mo) and vanadium (V), as well as hazardous heavy metals like as tungsten (W) and zinc[56]. It is difficult to fully understand that which siderophore moieties of *A. vinelandii* use to hold iron and how they work with Fe. More research is needed to figure out how these siderophores protect plants from pathogens and have anti-phytopathogenic properties, which will help in healthy growth of plants. When nitrogen is given, *A. vinelandii* siderophores can stimulate the growth of freshwater algae in co-culture[57]. Attention also required on investigations about the potential applications of such siderophores in promoting algal cultivation and enhancing nutrient availability for algae. The siderophore metabolome was also characterised and found over 35 metal-binding secondary metabolites that indicated *A. vinelandii's* large chelome which included vibrioferrin, previously found only in marine bacteria[54]. *A. chroococcum* produces vibrioferrin, amphibactins, and the novel siderophores crochelins[58]. Despite its agricultural value, *A. chroococcum's* secondary metabolome is likely to be unknown. The structures of siderophores and how *A. chroococcum* obtains Fe to produce high levels of nitrogenases are remain unexplored [59]. Determining the structures of the siderophores produced by *A. chroococcum* and their comparison with *A. vinelandii's* siderophores could provide insights into the diversity and functional roles of siderophores in these bacteria.

3. **Pesticide Degradation:** *Azotobacter* may degrade several aromatic compounds, including protocatechuic acid, p-hydroxy benzoate,2,4-D, benzoate and 2,4,6-trichlorophenol[60]. A study by Gaofeng et al. revealed that *Azotobacter* sp. degrades 2-chlorophenol, 4-chlorophenol, 2,6-dichlorophenol, and 2,4,6-trichlorophenol[61]. Notably, 2,4-D is the only substantial carbon source for *A. chroococcum*[62]. The specific enzymatic pathways and mechanisms involved in these degradation processes are not fully understood. Further research is needed to elucidate the metabolic pathways used by *Azotobacter* to degrade these compounds. Understanding the optimal conditions for aromatic derivative degradation by *Azotobacter* could be valuable for practical applications. Research could focus on identifying the factors that enhance degradation efficiency, such as temperature, pH, substrate concentration, and co-factors. *A. chroococcum* strains degrade lindane ex situ and in situ at 10 ppm. Bacteria degraded lindane less at higher concentrations. The capability of *A. chroococcum* to degrade

lindane in situ at 10 ppm is promising for environmental remediation[63]. However, further research is needed to explore the feasibility and effectiveness of using *A. chroococcum* in real-world applications for the bioremediation of lindane-contaminated sites. Lindane may inhibit bacterial growth at higher concentrations [64]. The observation that lindane may inhibit bacterial growth at higher concentrations raises questions about the toxicological effects of lindane on *Azotobacter* and other microorganisms. Investigating the mechanisms of lindane toxicity and its impact on microbial communities can help understand the limitations and challenges of using *Azotobacter* for lindane biodegradation. Kole et al. (1994) showed that *A. chroococcum* can convert pendimethalin, a common herbicide, into non-toxic products, proving that the bacterium is vital to crop production and environmental harmony[65]. We need further studies to validate this finding and explore the broader potential of using *A. chroococcum* for herbicide bioremediation.

4. **Plant Disease Control:** In a study conducted by Maheshwari et al. in 2012, it was demonstrated that the strain TRA2 of *A. chroococcum*, isolated from the wheat rhizosphere, displayed robust antagonistic activity against the root rot fungus *Macrophomina phaseolina* and *Fusarium oxysporum*[66]. Moreover, the presence of this strain resulted in enhanced wheat plant growth attributed to improved plant health. The mechanisms by which they exert this activity are not fully understood. Therefore, it is needed to identify the key antimicrobial compounds and growth hormones produced by *A. chroococcum* and their roles in suppressing plant diseases. There are likely multiple factors influencing the ability of *A. chroococcum* to suppress plant diseases, including the bacterial strain, environmental conditions, and the specific pathogen and target plant. Investigating these factors and their interactions could provide valuable insights into optimizing disease suppression strategies using *A. chroococcum*. Azotobacter exhibits a vigorous colonization of wheat roots, effectively safeguarding the plants. Akram et al. in 2016 discovered that *A. chroococcum* played a role in reducing root knot nematode (*Meloidogyne incognita*) disease in chickpea plants[67]. The control of plant diseases by bacteria involves various mechanisms, including the production of siderophores, antimicrobials, toxins, and growth hormones such as auxins, gibberellins, and cytokinins. However, the specific mechanisms employed depend on factors like the bacterial strain, environmental conditions, pathogen, and target, leading to diverse approaches in disease suppression. Verma et al. in 2001 demonstrated that *A. chroococcum* strains produce antimicrobial/antifungal substances *in vitro*[68]. The practical effectiveness of *A. chroococcum* in disease control can be further assessed through greenhouse and field trials. Many of the antimicrobial substances are extracellular, while a few are cell wall-bound. *Azotobacter* species can also produce siderophores that bind to available iron in the rhizosphere, depriving phytopathogens of this essential nutrient and protecting the plants[6]. Moreover, *Azotobacter* can synthesize anisomycin, a well-known fungicidal antibiotic[69]. Furthermore, *Azotobacter* bioinoculants have demonstrated the ability to manage various pathogens such as *Alternaria, Fusarium, Rhizoctonia, Macrophomina, Curvularia, Helminthosporium*, and *Aspergillus*[70]. In future, one can focus on the integration of *A. chroococcum* into IPM approaches, combining its disease-suppressive properties with other biological, cultural, and chemical control measures for a comprehensive and sustainable disease management strategy.

IV. BACILLUS SUBTILIS AS GROWTH PROMOTER, STRESS MANAGER AND IMMUNITY BOOSTER FOR HORTICULTURE PLANTS

Bacillus subtilis, a well-known rhizobacterium that forms biofilms, plays a crucial role in supporting plant health and promoting plant growth. Recent studies have unveiled its significant influence on various aspects of plant development, stress tolerance, and immune response, making it a promising tool to enhance global food production[71]. One of the key contributions of *B. subtilis* to plant growth lies in the production of volatile organic compounds (VOCs) like albuterol and 1,3-propanediol. Particularly, VOCs produced by *B. subtilis* SYST2 have been observed to stimulate plant growth by enhancing photosynthetic activity and phytohormone production[72].

Moreover, *Bacillus* species assist wheat plants in their photosynthetic processes by producing siderophores that chelate iron and supply this vital element to the plant's photosynthetic machinery[73]. The acidification triggered by the secretion of siderophores by *Bacillus* species is especially significant, as it makes previously inaccessible forms of various nutrients available to the plant. This leads to improved nutrient uptake and overall plant health [74]. The ability of the plant's roots to mediate processes like chelate degradation and ligand exchange reaction further facilitates the acquisition of nutrients from nutrient-siderophore complexes[75]. *B. subtilis* stands out for its highly organized genome and strong metabolic capabilities, allowing it to effectively withstand a wide range of abiotic stresses[76]. The bacterium possesses numerous genes that support plants in adapting to and coping with environmental stresses[77]. Spx, known for its binding to the alpha subunit of RNA polymerase, plays a central role in regulating stress responses [78]. Additionally, alarmones, acting as secondary messengers of nutrient scarcity, act as effective intermediates in safeguarding plant cells from heat shock and other stresses[79]. The cellular stress response of *B. subtilis* is intricate, and the role of (p)ppGpp in the heat shock response sheds light on some of its mechanisms. The study alamone investigated the central role of alarmone (p)ppGpp and the SR-like response in the heat shock response. The research demonstrated that (p)ppGpp levels significantly increased during heat shock but returned to baseline after 10 minutes[80]. Notably, the immediate effect of this spike in (p)ppGpp levels is to limit and modulate translation in response to heat stress, which reduces the protein burden on the quality control system while still enabling the expression of heat shock genes. The study highlighted Rel as the primary source of (p)ppGpp during heat stress, emphasizing its crucial role in the survival of *B. subtilis* cells under various stress conditions. Both Spx and (p)ppGpp were explored as potential mediators of the heat shock response, with the findings suggesting that one or the other is essential for optimal development under high-temperature conditions. The stress response mechanisms in *B. subtilis* are complex, evident from the discovery that even with a defective ribosome and decreased translation rate, survival under heat stress can still increase in the absence of the alarmone[81]. The study indicates that (p)ppGpp regulates global changes in translation rate to enhance stress tolerance, possibly affecting specific groups of proteins in the proteome. Understanding the stress signalling pathways and the protective effects of (p)ppGpp on translation under proteotoxic stress conditions may be aided by recognizing that (p)ppGpp plays a critical role in maintaining the integrity of ribosomal subunits and the formation of 100S particles under heat stress[82]. Interestingly, this study raises questions for future research, including the molecular mechanisms underlying the activation of Rel and the regulation of the SR in response to heat stress. There may be applications in organic farming and biotechnology if we can learn more

about the mechanisms involved in stress signalling. However, there are some holes in the research. It is not entirely clear, for example, how heat stress is sensed and communicated to Rel on the ribosome. Finding which tRNA molecules are involved in relaying the heat stress signal could shed light on this phenomenon. Further insight into *B. subtilis's* overall stress response may be gained by investigating the role of other heat stress-sensing proteins. Hence the study of (p)ppGpp and its function in stress responses has potential applications in organic farming. For instance, it could aid in the research and development of genetic engineering or other targeted stress management strategies to improve crop tolerance to stress. Uncovering the underlying molecular mechanisms may help scientists think of new ways to make agricultural systems more robust in the face of environmental stresses.

B. subtilis, when combined with arbuscular mycorrhizal fungi (AMF), has demonstrated a synergistic effect in mitigating the adverse impacts of salinity stress on plant metabolism. This beneficial cooperation is achieved through the production of glycine, betaine, and proline[83]. Moreover, *Bacillus* species possess a variety of genes, including KatA, SodA, trxA, and perR, which actively contribute to shielding plants from oxidative stress[84]. Additionally, the expression of genes such as DegS, dpsU20, desk, desR, and ResD by *Bacillus spp.* plays a pivotal role in safeguarding plants against the detrimental effects of cold stress[85]. While the synergistic effect of *B. subtilis* and AMF in alleviating salinity stress on plant metabolism is mentioned, the specific molecular and physiological mechanisms behind this synergy remain unclear. Future research should focus on understanding the interactions between these microorganisms and the plant's root system to elucidate how they work together to enhance plant stress tolerance. *Bacillus* strains with psychotropic properties have been the subject of investigation for their potential role in maintaining plant osmotic homeostasis. Several osmotic regulatory genes, such as opuAC and ohR, have been identified, and through increased peroxidase (POD) enzyme expression, they enhance plant survival during abiotic stress, mitigating the impact of unfavourable agroclimatic conditions[86]. This highlights the potential of utilizing *Bacillus* species to regulate plant responses to abiotic stress, ultimately benefiting global food production.

Bacillus species produce various phytohormones, including auxin, cytokinin, and expansin, which play a crucial role in stimulating plant growth[87]. Moreover, *Bacillus spp.* possess ACC deaminase genes that reduce plant ethylene levels, resulting in improved growth and drought tolerance[88]. Volatile organic compounds (VOCs) produced by *Bacillus,* such as 2-ethyl hexanol, tetrahydrofuran-3-ol, and 2-heptanone, interact with various compounds to promote plant growth[89]. These VOCs also have a significant impact on endogenous auxin levels and strigolactone production, modulating regulatory pathways in associated plants. The specific VOCs and their individual effects on plant growth and hormonal regulation need further investigation. Identifying and characterizing these VOCs will provide valuable insights into their potential use in organic farming.

The undeniable advantages of immune regulation and growth enhancement in plants induced by *Bacillus spp.* have garnered significant interest. When triggered by pathogen-related signals, primed plants increase the production of reactive oxygen species (ROS), the expression of defense-related genes, callose deposition in cell walls, and the synthesis of phytoalexins [90]. *Bacillus spp.* have been shown to induce ISR (Induced Systemic Resistance) in plants, collectively promoting plant growth and providing defense against various soil pathogens[91]. ISR signaling pathways differ from those of SAR (Systemic

Acquired Resistance), with ISR utilizing the ethylene/jasmonate pathway and the regulatory gene NPR1, while SAR employs the salicylic acid signalling pathway and the accumulation of pathogenesis-related proteins [92]. Specific *Bacillus strains,* such as *B. subtilis* S499 and *B. subtilis* CtpxS2-1, have been identified as inducers of ISR in beans and *Andean lupin*, respectively[93]. The immune regulation and enhancement induced by *Bacillus spp.* through ISR are promising. However, the precise signalling pathways involved in activating ISR and the crosstalk between ISR and other defence mechanisms need to be thoroughly studied. Understanding these pathways will aid in optimizing the induction of systemic resistance for better protection against pathogens in organic farming.

Moreover, the formation of biofilms in the root rhizosphere enhances the rhizo-competence of *Bacillus* species. PGPR (Plant Growth-Promoting Rhizobacteria) with the ability to form biofilms, such as *B. subtilis,* have demonstrated encouraging outcomes in increasing crop yield through diverse plant growth mechanisms[94]. To harness their potential, it is essential to investigate the molecular mechanisms underlying biofilm formation and how these biofilms interact with plant roots. This knowledge can be utilized to develop targeted strategies for enhancing plant-microbe interactions in the rhizosphere. Interestingly, PGPR-produced plant growth regulators and antimicrobials positively regulate plant metabolic pathways[95]. *B. subtilis* produces YIT toxin through the yitPOM operon, which acts as a biocontrol agent, competing with other microbes and benefiting plants[96]. Inoculating with nitrogen-fixing microbes further enhances the efficacy of these biofertilizers[97]. The root rhizosphere biofilm plays a crucial role in maintaining a balance between biotic and abiotic stresses, and *B. amyloliquefaciens* biofilms have been found to improve barley salt stress tolerance [98]. Much of the current research on *Bacillus spp.* and their effects on plant growth and stress tolerance is conducted in controlled laboratory settings. Future studies should focus on validating these findings in field conditions to assess their practical applicability in organic farming on a larger scale.

V. RHODOPSEUDOMONAS PALUSTRIS AS POTENTIAL BIOFERTILIZER FOR SUSTAINABLE AGRICULTURE

The changing climate poses negative impacts on agricultural output, with rising temperatures, increased precipitation, and extreme weather events leading to reduced crop yield and changes in pest and weed growth patterns[99]. While some pests and pathogens may decline due to higher temperatures, the overall effect on crop production is concerning due to short-term failures and long-term declines caused by alterations in precipitation intensity and frequency[100]. To address salinity stress, heavy metal stress, and greenhouse gas emissions, while enhancing the yield and quality of edible plant parts, the presence of phototropic purple non-sulfur bacteria (PNSB) can be beneficial[101]. *R. palustris*, a PNSB bacterium, has shown potential in improving plant development and productivity[102]. In the context of rice crops, field evaluations based on parameters like plant height, tiller number, leaf chlorophyll content, and lodging resistance revealed positive effects of PNSB treatment[103]. Plants treated with PNSB exhibited steady growth in height, outperforming untreated plants at every stage of development. The treatment resulted in increased plant height, tiller count, leaf chlorophyll content, lodging resistance, and dry mass of rice[103]. The current findings focus on rice crop performance, but to establish the versatility of *R. palustris* as a biofertilizer, it is essential to conduct field trials with a wide range of crops. Different crops may respond differently to PNSB treatment, and understanding this variation

is crucial for its practical application in diverse agricultural systems. The study mentioned above appears to be a short-term evaluation of PNSB effects on rice crops. To assess the long-term impacts and sustainability of PNSB as a biofertilizer, it is necessary to conduct studies over multiple cropping seasons. This will help determine if the positive effects observed in the short term are consistent and enduring. Because of its biodetoxification and biodegradation properties, *R. palustris* can be used to process animal and industrial waste which is hugely available in the agriculture land[104]. The presence of multiple ring cleavage pathways in its genome is further evidence of its exceptional biodegradation abilities. This bacterium has the potential to serve as a source for biopolymers and building blocks due to the production of useful chemicals such as PHB, polysaccharides, and isoprenoids. *R. palustris*, a biofertilizer commonly used in agriculture, reduces contaminant levels in the soil and improves soil quality[105]. By cloning its genes into plants, heavy metals and pesticides can be tolerated and degraded. In addition, *R. palustris* stimulates development in plants by fixing nitrogen and making phytohormones[106]. It improves plants' immune response and makes them more resistant to diseases like tobacco mosaic virus. *R. palustris* shows great promise as a potential biofertilizer in agriculture due to its wide range of properties, which include detoxification, degradation, plant growth promotion, and antiviral abilities[107]. To successfully implement *R. palustris* as a biofertilizer in agriculture, understanding farmers' attitudes, perceptions, and barriers to adoption is crucial. Social and economic research can provide insights into promoting its acceptance among farmers and ensuring its successful integration into farming practices.*R. palustris* PS3 and YSC3, two closely related bacterial strains, were the focus of a study looking at how they affect the development of Chinese cabbage. In contrast to PS3, which promoted greater shoot and root biomass in plants, YSC3 had no such effect. Leaf area expansion, rather than an increase in leaf number, was the primary contributor to the increased shoot biomass in PS3-treated plants[108]. However, the study established that PS3 promotes plant growth and enhances shoot and root biomass, the specific mechanisms by which this bacterium exerts its positive effects remain largely unknown. Further research could investigate the specific plant growth-promoting traits and molecular mechanisms employed by PS3 to stimulate leaf area expansion and overall biomass accumulation in Chinese cabbage. Furthermore, plants that were inoculated with PS3 showed enhanced nitrate uptake and nitrogen use efficiency (NUE). They drank more of the hydroponic solution, resulting in a lower level of residual nitrate. The upregulation of the nitrate transporter gene NRT1.1 was linked to the improvement in NUE[108]. It would be helpful to design microbial inoculants that improve crop plants' nitrogen uptake efficiency if we knew which genes and pathways were involved in this process. PS3 inoculation also increased cell proliferation in young leaves, a key factor in promoting leaf growth[109]. Auxin (IAA) is a plant hormone. PS3 was more sensitive to chemoattractants or chemorepellents derived from root exudates, while YSC3 showed a different response to the rhizosphere environment of the host plant[110]. These results shed light on the intricate relationships between bacteria and plants and could help farmers develop more effective methods of encouraging plant growth. The importance of understanding the interactions between beneficial bacteria and root exudates is highlighted by the fact that PS3 and YSC3 react differently to chemoattractants and chemorepellents derived from root exudates. Understanding the communication and recognition mechanisms that mediate plant-microbe interactions may require elucidating the specific compounds in root exudates that elicit different responses from these strains.

VI. OTHER IMPORTANT BACTERIA AND PROJECTED APPLICATIONS IN PLANT GROWTH PROMOTIONS

A vast array of plant growth benefits could also be provided by bacteria's still remaining unexplored after the continuous research of past several decades. Therefore, exploration of uncharacterized plant commensal microbes essentially required. In this section we have attempted highlight the importance of few more bacteria which come under observation by indicative initial experiment for particular unique properties of bacteria. Where, siderophores are highlighted at various places to provide improved plant immunity and health. According to a 2007 research by Miethke and Marahiel, siderophores can be categorised as phenolate, hydroxamate, catecholate, (hydroxy-)carboxylate, and mixed forms. The production of siderophores requires several pathways[111]. Within the *Rhodococcus* spp. strains, several chemically distinct siderophores have been found, such as rhodochelin, rhodobactin, heterobactin A, rhequichelin, and rhequibactin[25]. Notably, Carrano et al. were among the first to isolate *R. erythropolis* heterobactins from IGTS8 culture in 2001[112]. Heterobactin A and B were determined to be the most abundant of these heterobactins[15]. Heterobactins are structurally categorised as catecholate-hydroxamate mixed-type siderophores because they include both hydroxamate and catecholate donor groups. Bosello et al. (2013) isolated heterobactins from *R. erythropolis* PR4 and effectively identified the gene cluster responsible for the manufacture of heterobactin A by bioinformatic analysis of the bacterial genome[113]. In the future researchers can further study the heterobactins produced by *R. erythropolis* PR4. The focus includes structural characterization, gene cluster analysis for biosynthesis, and gene expression studies under different conditions. We can also target the functional role of heterobactins, such as their ability to sequester iron and their impact on microbial interactions. Additionally, the ecological significance of heterobactins in influencing microbial communities and their potential biotechnological applications can be explored. Each nonribosomal peptide synthetase (NRPS) module contributes a particular monomer to the peptide backbone during the production of heterobactin Doroghazi and Metcalf's 2013 genomic analysis of four *Rhodococcus rhodochrous* strains indicated a disproportionate amount of gene clusters encoding NRPSs compared to other Actinobacteria[114]. Rhodochelin and rhodobactin are classed as hydroxamate-catecholate mixed-type siderophores, comparable to heterobactin. In 2007, Dhungana et al. and Bosello et al. isolated them from *Rhodococcus jostii* RHA1 and *Rhodococcus* rhodochrous OFS, respectively[115]. Although the gene clusters involved in rhodobactin synthesis have not been found, RHA1 describes the gene clusters involved in rhodochelin synthesis[116]. In addition, research indicates that siderophores generated by *R. erythropolis* S43 have a greater affinity for binding trivalent arsenic (As(III)) than iron chelation[117]. As stated by Retamal-Morales et al. in 2018b, this fascinating arsenic-binding activity of siderophore-like compounds from S43 has prospective implications in soil and water purification and other biotechnological applications[118]. Each NRPS module contributes a particular monomer to the peptide backbone during the production of heterobactin. Doroghazi and Metcalf's (2013) carried out the genomic analysis of four *Rhodococcus* strains indicated a disproportionate amount of gene clusters encoding NRPSs compared to other Actinobacteria[114]. Rhodochelin and rhodobactin are classed as hydroxamate-catecholate mixed-type siderophores, comparable to heterobactin. In 2007, Dhungana et al. and Bosello et al. isolated them from *R. jostii* RHA1 and *R. rhodochrous* OFS, respectively[119]. Although the gene clusters involved in rhodobactin synthesis have not been found, RHA1 describes the gene clusters involved in rhodochelin synthesis. In addition, research indicates that siderophores

generated by *R. erythropolis* S43 have a greater affinity for binding trivalent arsenic (As(III)) than iron chelation[120]. As stated by Retamal-Morales et al. in 2018b, this fascinating arsenic-binding activity of siderophore-like compounds from S43 has prospective implications in soil and water purification and other biotechnological applications[118]. Additional research into siderophores in the agricultural context could examine how they are taken up by plants, how they affect the uptake of crucial micronutrients, and whether or not they can synergize with mycorrhizal associations. It is crucial to conduct large-scale field trials to assess the long-term effects on crop yield and soil health, as well as to determine whether or not siderophores are compatible with organic farming practises. Sustainable agriculture can benefit from research into the role of siderophores in plant-microbe interactions and their possible use in boosting crop resistance to stress. Genetic engineering of *Rhodococcus* strains to maximise siderophore production has the potential to yield environmentally friendly and productive agricultural practises that boost nutrient uptake, plant growth, and soil health with minimal negative effects on the surrounding ecosystem. The regulation of bacterial iron uptake is controlled by the Fur box, a protein that responds to iron concentrations. At high iron levels, the Fur protein binds to the siderophore gene promoter, preventing the production of siderophores[121]. However, when intracellular iron is low, the Fur protein detaches from the promoter, allowing gene transcription and siderophore synthesis[122]. Pyoverdine, a siderophore produced by *P. fluorescens*, enhances its virulence and pathogenicity[123]. Interestingly, pyoverdine has also been found to improve iron nutrition in tomato plants, suggesting its potential as a biofertilizer[17]. Scientists can genetically manipulate the Fur regulatory system in bacteria to increase siderophore production and agricultural benefits. In the future we could fine-tune siderophore synthesis if we knew how the Fur protein bound and detached from the gene promoter. Additionally, understanding how bacteria that produce siderophores like pyoverdine interact with different plant species can help us modify siderophores for individual crops to increase iron nutrition. We can also engineer bacteria to produce siderophores with improved stability, iron chelation, and root colonisation, which could lead to more efficient biofertilizers. These findings could lead to environmentally friendly and productive agricultural practises that use natural siderophores to improve nutrient uptake, crop yield, and fertiliser use.

Mst 8.2, a strain of *P. fluorescens*, has shown inhibitory effects on fungal pathogens and has been effective in reducing root rot lesions and improving wheat plant growth[124]. Further analysis through 16S rRNA sequencing confirmed the link between Mst 8.2 and *P. fluorescens*[125]. *Alcaligenes faecalis*, a rhizobacterium found in groundnuts, produces siderophores that enhance seed germination, root and shoot length, as well as chlorophyll content[126]. To maximise agricultural benefits, Mst 8.2 and *A. faecalis'* mechanisms of action and genetic basis must be understood. Genomic and transcriptomic analyses of beneficial strains can reveal the genes and pathways that suppress fungal pathogens, reduce root rot lesions, and boost plant growth. We must identify and characterise genes that produce antifungal compounds and siderophores to develop genetically modified crops with improved pathogen resistance and nutrient uptake. Mst 8.2 and *A. faecalis* root-microbe interactions can illuminate seed germination, root and shoot growth, and chlorophyll synthesis signalling pathways. Using this information, we can develop plants that are genetically predisposed to attract and interact with beneficial rhizobacteria, increasing plant vitality and productivity. CRISPR-Cas9 allows precise manipulation of plant genomes to improve their symbiotic relationships with these helpful bacteria. Molecular biology can unlock the full potential of

Mst 8.2 and *A.s faecalis*, resulting in more sustainable, resilient, and productive crop production systems with fewer chemical inputs.

The Rhizobacterium *Cellulosimicrobium* sp. has been identified as a barley-growth-promoting bacterium. It produces antibiotics, siderophores, and enzymes, effectively inhibiting pathogens such as *Botrytis, Fusarium, and Verticillium.*This bacterium exhibits biocontrol and inoculant potential[127]. Fusarinines and dimerium acid from *Penicillium chrysogenum* have been found to aid plants in utilizing iron, resulting in increased chlorophyll concentration and iron content in plants such as cucumber and maize[128]. Iron-deficient plants showed improved growth when treated with siderophore mixtures or hydrolysates. Bacillibactin, another siderophore, has been investigated for its potential in agricultural biocontrol *Bacilibactin,* another siderophore, has been investigated for its potential in agricultural biocontrol[129]. Studies have shown that *B. subtilis*, a siderophore-producing bacterium, can prevent *Fusarium* wilt and promote pepper growth[130]. It also demonstrated biocontrol capabilities against the red pepper blight pathogen *Phytophthora capsici*[131]. Additionally, certain siderophores produced by *P. azotoformans* were found to have the ability to decontaminate arsenic-contaminated soil[17]. Siderophore-producing strains of *P. aeruginosa*, *P. fluorescens*, and *Ralstonia metallidurans* were found to enhance the phytoremediation of chromium (Cr) and lead (Pb) when inoculated in maize plants[132]. These findings suggest the potential of siderophores in improving the removal of heavy metals from contaminated soil. Exploring the mechanisms of action of *Cellulosi microbium* sp. and other siderophore-producing bacteria in pathogen inhibition, optimising production via genetic engineering, studying plant-microbe interactions, developing novel application methods, and investigating their effects on a wider range of crops are all possible avenues for future study. Maximizing the potential of siderophore-producing bacteria for agricultural applications leads to better crop growth, disease resistance, and sustainable farming practises; further research can focus on optimising phytoremediation for heavy metals, assessing their environmental impact, and developing targeted biocontrol strategies for crop protection.

VII. CONCLUSIONS

In conclusion, the research on *Rhodococcus* strains, *Azotobacter, B. subtilis*, and other helpful bacteria shows how much biotechnology has the potential to change sustainable agriculture. These microorganisms have many benefits, such as making biosurfactants, promoting growth, reducing stress, boosting immunity, and breaking down pollutants. Using biotechnology to make the most of their abilities can help solve important problems in modern agriculture, such as climate change, soil degradation, and pollution. One must look to the future, where forecasting the biotechnology and its use in sustainable agriculture are likely to make even more progress. Techniques like genetic engineering, precision editing, and metabolic engineering will continue to be very important for improving beneficial microbial strains and making them fit the needs of agriculture. This will lead to better biofertilizers, biocontrol agents, and biosurfactants that are better for the environment, cost less, and can be made to fit different crops and farming methods. Research that combines biotechnology, microbiology, agronomy, and environmental sciences will help us learn more about how microorganisms and plants interact with each other. This information will help scientists come up with new ways to encourage plant-microbe symbiosis, improve nutrient cycling, to improve soil health, which will lead to sustainable and regenerative farming practises. The commercial viability of microbial products in agriculture will also be helped by

finding new carbon sources, fine-tuning growth media formulations, and making in fermentation processes as efficient as possible. Using waste materials as substrates for microbial production not only saves money, but also supports the idea of a circular economy and protects the environment. Biotechnological advances have a lot of potential to help solve the world's problems with food security, climate change, and protecting the environment in the future. By combining helpful microorganisms with cutting-edge biotechnology, we can make an agricultural landscape that is more resilient, eco-friendly, and productive. In such way bio-organic/eco-friendly solutions will help to feed growing population while protecting the planet's natural resources. However, intensive approaches required to know more about the game-changing technologies for enhanced growth of sustainable agriculture to bring people and healthy environment together.

VIII. ACKNOWLEDGEMENTS

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